on magnetosome island, magnetotactic islet, flagellar, and cytoskeleton genes. AMB-1 cultures were subjected to static, high magnetic field (10G) generated by a solenoid or to low frequency pulsed magnetic field (between 0G and 10G at 0.0033 Hz) for 30 min, 1 hour, 3 hours or 6 hours. After extracting total RNA and converting to cDNA, quantitative real time-PCR was performed to measure relative transcription levels. Both static and pulsed magnetic fields altered gene expression with the greatest changes occurring at shorter time points. Differential regulation of *mamK* and *mamK-like* genes responsible for mechanical stabilization of magnetosomes, in addition to flagellar anchor protein *fliF* and actin-like structural protein *mreB*, provides evidence for altered regulation of mechanics- and motility-related processes with magnetic activation. We believe these findings provide significant targets for understanding the genetic regulation and mechanics of magnetically-driven bionavigation.

3291-Pos Board B446
Mechanochemistry of Focal Adhesion Dynamics
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Focal adhesions (FA) are ''feet'' of the cell that mediate cell migration on extracellular matrix (ECM). FA formation involves the crosstalk between mechanical cues (*e.g.*, ECM stiffness and actomyosin contractile forces), and biochemical signaling events (e.g., the mechanosensitivity of focal adhesion components). However, the coherent physical mechanism that governs mechanochemistry of FA formation is still missing. We established a coherent model that focuses on the mechanochemstry of focal adhesion dynamics. Our model captures the essential characteristics of focal adhesion dynamics. In particular, the model accounts for the mechanosensation of focal adhesion growth at different ECM rigidities, asymmetrical distribution and the oscillations of traction force within FA. Our model provides an integrated perspective of the focal adhesion dynamics and the roles in mechanosensing during the cell migrations.

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Dynamics and Force Generation by Single Motor Complexes in M. Xanthus
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The gram-negative bacterium Myxococcus xanthus is an important model system for multicellular group formation. These cells move on solid surfaces using a combination of gliding and twitching motility. Whereas pilus retraction drives twitching, the mechanism controlling gliding is not fully understood. We recently identified a new class of molecular motors that power gliding motility [1]. These motors, AglQRS proton channels, assemble within focal adhesion sites that are separated by approximately 480nm along the cell [2]. It is currently unknown how much force the motors can generated and whether they act individually or in cooperative groups.
Here, we combined optical tweezers and real-time tracking of motor-driven beads to address these topics. We find that gliding motors produce saltatory movements on two major time scales, 0.4s and 3.5s. These are likely associated with motor kinetics and cargo binding respectively. During bursts of motor activity, we applied a controlled load to slow single motor movement along the cell axis. We show that mechanical force is sufficient to reduce the velocity of a gliding motor complex and that motors stall under forces stronger than 12pN. We reduced the pH gradient through exposure to mild concentrations of the drug nigericin. We find that the characteristic force is independent of the driving proton motive force.
[1] Sun et al., PNAS(108)7559, 2011. [2] Mignot et al., Science(315)853, 2007.

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Are "Power-Packs" Associated with the Switch-Motor Complex of Bacterial Flagella?
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Bacterial flagella are rotated by a motor embedded in the cytoplasmic membrane, the direction of rotation being dictated by a switch at the base of the motor. In the case of bacteria such as *E.coli* and *Salmonella*, the motor is driven by the proton-motive force (PMF) across the membrane. The PMF is also used, *inter alia*, to synthesize ATP by means of the reversible membrane enzyme F_0F_1ATPase, whose mechanism involves the rotary action of a spindle. Recently, the switch-motor complex of bacterial flagella was found to be associated with a number of non-flagellar proteins, which, in spite of not belonging to the chemotaxis system, affect the function of the flagella. The observation that one of these proteins, fumarate reductase, is involved in electron transport under anaerobic conditions raised the question of whether other energy-linked enzymes are associated with the switch-motor complex as well. Here, we identified two additional such enzymes in *E.coli*. Employing F**ö**rster resonance energy transfer in vivo and pull-down assays in vitro, we provided evidence for the interaction of F_0F_1ATP synthase via its β subunit with the flagellar switch protein FliG and for the interaction of NADH-ubiquinone oxidoreductase with FliG, FliM, and possibly FliN. Furthermore, we measured higher rates of ATP synthesis, ATP hydrolysis, and electron transport from NADH to oxygen in membrane areas adjacent to the flagellar motor than in other membrane areas. All these observations suggest the association of energy complexes with the flagellar switch-motor complex. Finding that deletion of the β subunit in vivo affected the direction of flagellar rotation and switching frequency further implied that the interaction of F_0F_1ATP synthase with FliG is important for the function of the switch of bacterial flagella.

3294-Pos Board B449
Switching Bacterial Flagella Motor
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The bacterial flagella motor stochastically switches between clockwise (CW) and counterclockwise (CCW) rotation. The switching of flagella motor is regulated by the signalling protein CheY-P whose concentration is governed by the bacterial chemotaxis signalling network. Experiments have shown that the switching of bacterial flagella motor is highly cooperative with a Hill coefficient around 10. We study first the switching behavior of flagella motor by analytical approach and kinetic Monte Carlo simulation. Dwell time statistics is characterized in comparison with experimental results. We next investigate dynamic properties of the motor switching under equilibrium or non-equilibrium condition. The switching dynamics is coupled to torque generation of the motor. Structural features of rotor are incorporated upon previous work. Stator-rotor interactions are in particular considered that may lead to experimentally observable effects.

3295-Pos Board B450
Structural Basis for the Specific Recognition of Dual Receptors by the Homopolymeric Psa Fimbriae of Yersinia Pestis
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The pH 6 antigen or Psa fimbriae of Yersinia pestis bind to two receptors, β1-linked galactosyl residues in glycosphingolipids and phosphocholine group in phospholipids. Despite the ubiquitous presence of either moiety on the surface of many mammalian cells, Y. pestis appears to prefer interacting with certain types of human cells such as macrophages and alveolar epithelial cells of the lung. The molecular mechanism of this apparent selectivity is not clear. Site-directed mutagenesis of the consensus choline-binding motif in the sequence of PsaA, the subunit of the Psa fimbrial homopolymer, identified residues that abolish either galactosylceramide or phosphatidylcholine binding or both. The crystal structure of the ternary complex of an in cis donor-strand complemented PsaA, galactose and phosphocholine reveals separate galactose and phosphocholine binding sites that share a common structural motif, thus suggesting potential interaction between the two sites. Mutagenesis of this shared structural motif identified Tyr126, which is part of the choline-binding consensus sequence but is found in direct contact with the galactose in the structure of PsaA, important for both receptor binding. This is the first structural resolution of a fimbrial subunit that forms a polymeric polyadhesin describing a unique arrangement of dual receptor binding sites. These findings move the field forward by providing insights into new types of multiple receptor-ligand interactions and should steer research into the synthesis of dual receptor inhibitor molecules to slow down the rapid progression of plague.